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```
  1 GAATTTGGCC CTCGAGGCCA AGAATTCGGC ACGAGGCGCG GCGCCCAGCG CAGGCAGAGC GCTGTCGCAT CCCGGGCGTC CACCCGCCAT GGGGCTCTCC
    CTTAAACCGG GAGCTCCGGT TCTTAAGCCG TGCTCCGCGC CGCGGGTCGC GTCCGTCTCG CGACAGCGTA GGGCCCGCAG GTGGGCGGTA CCCCGAGAGG
  1                                                                                                  Me tGlyLeuSer

101 TGGAGCCCGC GACCTCCACT GCTGATGATC CTGCTACTGG TGCTGTCGTT GTGGCTGCCA CTTGGAGCAG GAAACTCCCT TGCCACAGAG AACAGGTTTG
    ACCTCGGGCG CTGGAGGTGA CGACTACTAG GACGATGACC ACGACAGCAA CACCGACGGT GAACCTCGTC CTTTGAGGGA ACGGTGTCTC TTGTCCAAAC
  5 TrpSerProA rgProProLe uLeuMetIle LeuLeuLeuV alLeuSerLe uTrpLeuPro LeuGlyAlaG lyAsnSerLe uAlaThrGlu AsnArgPheVal

201 TGAACAGCTG TACCCAGGCC AGAAAGAAAT GCGAGGCTAA TCCCGCTTGC AAGGCTGCCT ACCAGCACCT GGGCTCCTGC ACCTCCAGTT TAAGCAGGCC
    ACTTGTCGAC ATGGGTCCGG TCTTTCTTTA CGCTCCGATT AGGGCGAACG TTCCGACGGA TGGTCGTGGA CCCGAGGACG TGGAGGTCAA ATTCGTCCGG
 39   AsnSerCy sThrGlnAla ArgLysLysC ysGluAlaAs nProAlaCys LysAlaAlaT yrGlnHisLe uGlySerCys ThrSerSerL euSerArgPro

301 GCTGCCCTTA GAGGAGTCTG CCATGTCTGC AGACTGCCTA GAGGCAGCAG AACAACTCAG GAACAGCTCT CTGATAGACT GCAGGTGCCA TCGGCGCATG
    CGACGGGAAT CTCCTCAGAC GGTACAGACG TCTGACGGAT CTCCGTCGTC TTGTTGAGTC CTTGTCGAGA GACTATCTGA CGTCCACGGT AGCCGCGTAC
 72  LeuProLeu GluGluSerA laMetSerAl aAspCysLeu GluAlaAlaG luGlnLeuAr gAsnSerSer LeuIleAspC ysArgCysHi sArgArgMet

401 AAGCACCAAG CTACCTGTCT GGACATTTAT TGGACCGTTC ACCCTGCCCG AAGCCTTGGT GACTACGAGT TGGATGTCTC ACCCTATGAA GACACAGTGA
    TTCGTGGTTC GATGGACAGA CCTGTAAATA ACCTGGCAAG TGGGACGGGC TTCGGAACCA CTGATGCTCA ACCTACAGAG TGGGATACTT CTGTGTCACT
105 LysHisGlnA laThrCysLe uAspIleTyr TrpThrValH isProAlaAr gSerLeuGly AspTyrGluL euAspValSe rProTyrGlu AspThrValThr

501 CCAGCAAACC CTGGAAAATG AATCTTAGCA AGTTGAACAT GCTCAAACCA GACTCGGACC TCTGCCTCAA ATTTGCTATG CTGTGTACTC TTCACGACAA
    GGTCGTTTGG GACCTTTTAC TTAGAATCGT TCAACTTGTA CGAGTTTGGT CTGAGCCTGG AGACGGAGTT TAAACGATAC GACACATGAG AAGTGCTGTT
139   SerLysPr oTrpLysMet AsnLeuSerL ysLeuAsnMe tLeuLysPro AspSerAspL euCysLeuLy sPheAlaMet LeuCysThrL euHisAspLys

601 GTGTGACCGC CTGCGCAAGG CCTACGGGGA GGCATGCTCA GGGATCCGCT GCCAGCGCCA CCTCTGCCTA GCCCAGCTGC GCTCCTTCTT TGAGAAGGCA
    CACACTGGCG GACGCGTTCC GGATGCCCCT CCGTACGAGT CCCTAGGCGA CGGTCGCGGT GGAGACGGAT CGGGTCGACG CGAGGAAGAA ACTCTTCCGT
172  CysAspArg LeuArgLysA laTyrGlyGl uAlaCysSer GlyIleArgC ysGlnArgHi sLeuCysLeu AlaGlnLeuA rgSerPhePh eGluLysAla

701 GCAGAGTCCC ACGCTCAGGG TCTGCTGCTG TGTCCCTGTG CACCAGAAGA TGCGGGCTGT GGGGAGCGGC GGCGTAACAC CATCGCCCCC AGTTGCGCCC
    CGTCTCAGGG TGCGAGTCCC AGACGACGAC ACAGGGACAC GTGGTCTTCT ACGCCCGACA CCCCTCGCCG CCGCATTGTG GTAGCGGGGG TCAACGCGGG
205 AlaGluSerH isAlaGlnGl yLeuLeuLeu CysProCysA laProGluAs pAlaGlyCys GlyGluArgA rgArgAsnTh rIleAlaPro SerCysAlaLeu

801 TGCCTTCTGT AACCCCCAAT TGCCTGGATC TGCGGAGCTT CTGCCGTGCG GACCCTTTGT GCAGATCACG CCTGATGGAC TTCCAGACCC ACTGTCATCC
    ACGGAAGACA TTGGGGGTTA ACGGACCTAG ACGCCTCGAA GACGGCACGC CTGGGAAACA CGTCTAGTGC GGACTACCTG AAGGTCTGGG TGACAGTAGG
239   ProSerVa lThrProAsn CysLeuAspL euArgSerPh eCysArgAla AspProLeuC ysArgSerAr gLeuMetAsp PheGlnThrH isCysHisPro

901 TATGGACATC CTTGGGACTT GTGCAACTGA GCAGTCCAGA TGTCTGCGGG CATACCTGGG GCTGATTGGG ACTGCCATGA CCCCAAACTT CATCAGCAAG
    ATACCTGTAG GAACCCTGAA CACGTTGACT CGTCAGGTCT ACAGACGCCC GTATGGACCC CGACTAACCC TGACGGTACT GGGGTTTGAA GTAGTCGTTC
272  MetAspIle LeuGlyThrC ysAlaThrGl uGlnSerArg CysLeuArgA laTyrLeuGl yLeuIleGly ThrAlaMetT hrProAsnPh eIleSerLys
```

FIG. 1A

```
1001 GTCAACACTA CTGTTGCCTT AAGCTGCACC TGCCGAGGCA GCGGCAACCT ACAGGACGAG TGTGAACAGC TGGAAAGGTC CTTCTCCCAG AACCCCTGCC
     CAGTTGTGAT GACAACGGAA TTCGACGTGG ACGGCTCCGT CGCCGTTGGA TGTCCTGCTC ACACTTGTCG ACCTTTCCAG GAAGAGGGTC TTGGGGACGG
 305 ValAsnThrT hrValAlaLe uSerCysThr CysArgGlyS erGlyAsnLe uGlnAspGlu CysGluGlnL euGluArgSe rPheSerGln AsnProCysLeu

1101 TCGTGGAGGC CATTGCAGCT AAGATGCGTT TCCACAGACA GCTCTTCTCC CAGGACTGGG CAGACTCTAC TTTTTCAGTG GTGCAGCAGC AGAACAGCAA
     AGCACCTCCG GTAACGTCGA TTCTACGCAA AGGTGTCTGT CGAGAAGAGG GTCCTGACCC GTCTGAGATG AAAAAGTCAC CACGTCGTCG TCTTGTCGTT
 339   ValGluAl aIleAlaAla LysMetArgP heHisArgGl nLeuPheSer GlnAspTrpA laAspSerTh rPheSerVal ValGlnGlnG lnAsnSerAsn

1201 CCCTGCTCTG AGACTGCAGC CCAGGCTACC CATTCTTTCT TTCTCCATCC TTCCCTTGAT TCTGCTGCAG ACCCTCTGGT AGCTGGGCTT CCTCAGGGTC
     GGGACGAGAC TCTGACGTCG GGTCCGATGG GTAAGAAAGA AAGAGGTAGG AAGGGAACTA AGACGACGTC TGGGAGACCA TCGACCCGAA GGAGTCCCAG
 372  ProAlaLeu ArgLeuGlnP roArgLeuPr oIleLeuSer PheSerIleL euProLeuIl eLeuLeuGln ThrLeuTrp

1301 CTTTGTCCTC TCCACCACAC CCAGACTGAT TTGCAGCCTG TGGTGGGAGA GAACTCGCCA GCCTGTGGAA GAAGACGCAG CGTGCTACAC AGCAACCCGG
     GAAACAGGAG AGGTGGTGTG GGTCTGACTA AACGTCGGAC ACCACCCTCT CTTGAGCGGT CGGACACCTT CTTCTGCGTC GCACGATGTG TCGTTGGGCC

1401 AACCAACCAG GCATTCCGCA GCACATCCCG TCTGCTCCAG AAGAGGTCTT AGAAGTGAGG GCTGTGACCC TTCCGATCCT GAGCGGCTAG TTTTCAAACC
     TTGGTTGGTC CGTAAGGCGT CGTGTAGGGC AGACGAGGTC TTCTCCAGAA TCTTCACTCC CGACACTGGG AAGGCTAGGA CTCGCCGATC AAAAGTTTGG

1501 TCCCTTGCCC CTGCTTCCTT CTGGCTCAGG CTGCTCCTCC TTAGGACTTT GTGGGTCCAG TTTTGCCTTC TGTTCTGATG GTGATTAGCG GCTCACCTCC
     AGGGAACGGG GACGAAGGAA GACCGAGTCC GACGAGGAGG AATCCTGAAA CACCCAGGTC AAAACGGAAG ACAAGACTAC CACTAATCGC CGAGTGGAGG

1601 AGCGCTTCTT CCTGTTTCCC AGGACCACCC AGAGGCTAAG GAATCAGTCA TTCCCTGTTG CCTTCTCCAG GAAGGCAGGC TAAGGGTTCT GAGGTGACTG
     TCGCGAAGAA GGACAAAGGG TCCTGGTGGG TCTCCGATTC CTTAGTCAGT AAGGGACAAC GGAAGAGGTC CTTCCGTCCG ATTCCCAAGA CTCCACTGAC

1701 AGAAAAATGT TTCCTTTGTG TGGAAGGCTG GTGCTCCAGC CTCCACGTCC CTCTGAATGG AAGATAAAAA CCTGCTGGTG TCTTGACTGC TCTGCCAGGC
     TCTTTTTACA AAGGAAACAC ACCTTCCGAC CACGAGGTCG GAGGTGCAGG GAGACTTACC TTCTATTTTT GGACGACCAC AGAACTGACG AGACGGTCCG

1801 AATCCTGAAC ATTTGGGCAT GAAGAGCTAA AGTCTTTGGG TCTTGTTTAA CTCCTATTAC TGTCCCCAAA TTCCCCTAGT CCCTTGGGTC ATGATTAAAC
     TTAGGACTTG TAAACCCGTA CTTCTCGATT TCAGAAACCC AGAACAAATT GAGGATAATG ACAGGGGTTT AAGGGGATCA GGGAACCCAG TACTAATTTG

1901 ATTTGACTT AAAAAAAAAA AAAAAAAAAA AAAAA
     TAAAACTGAA TTTTTTTTTT TTTTTTTTTT TTTTT
```

FIG. 1B

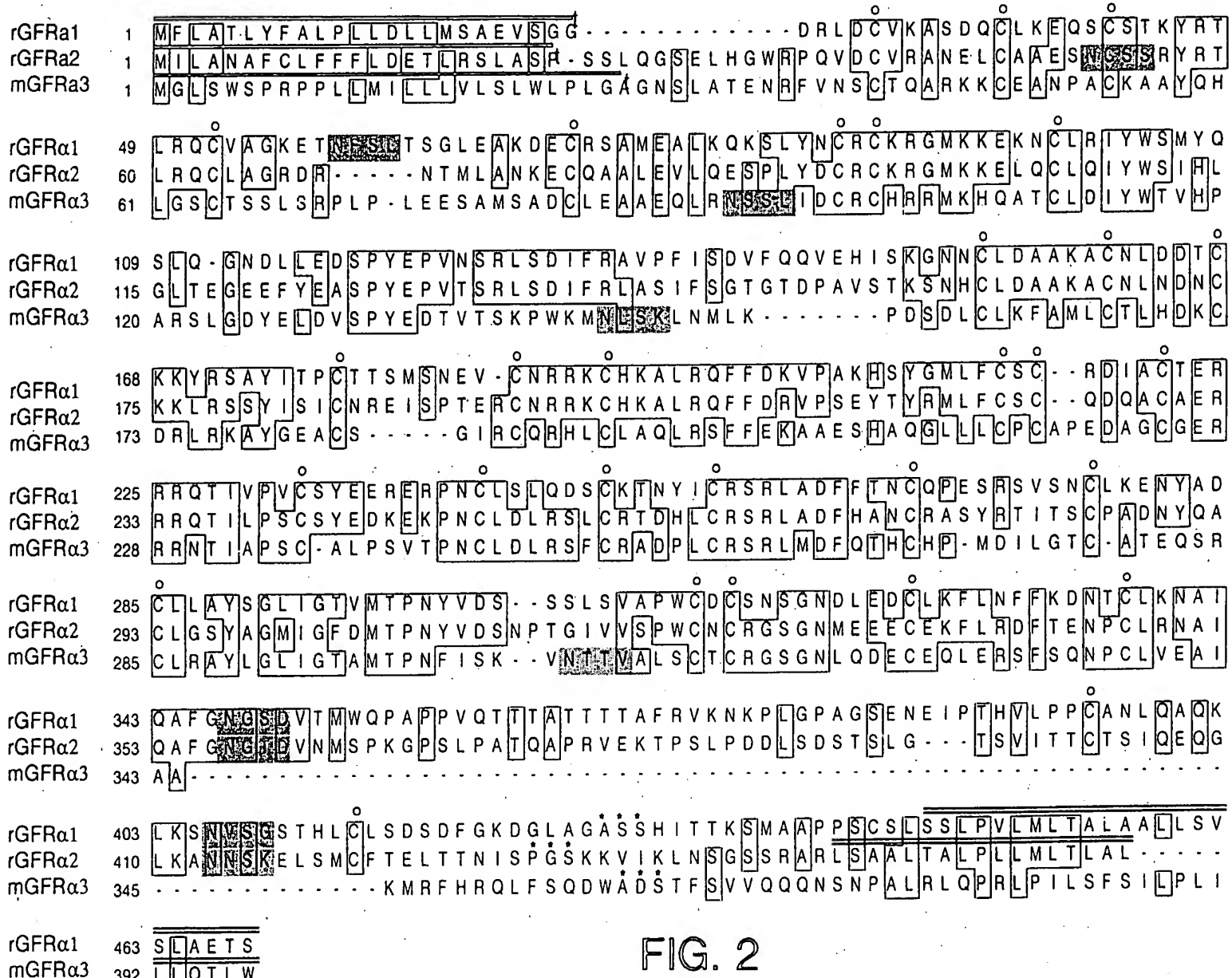

FIG. 2

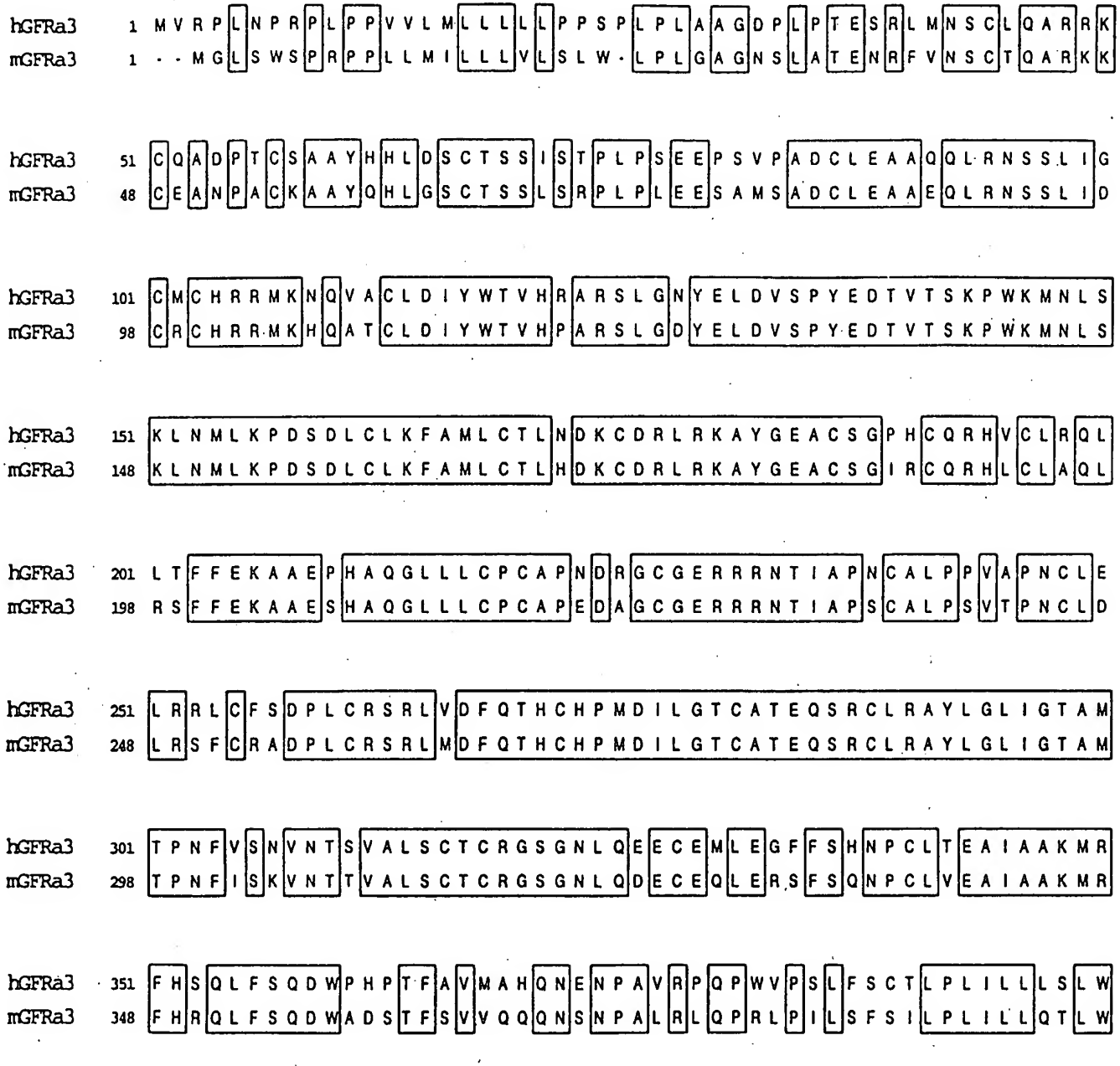

FIG. 3

```
48613     1 MVRPLNPRPLPPVVLMLLLLLPPSPLPLAAGDPLPTESRLMNSCLQARRK
48614     1 MVRPLNPRPLPPVVLMLLLLLPPSPLPLAAGDPLPTESRLMNSCLQARRK

48613    51 CQADPTCSAAYHHLDSCTSSISTPLPSEEPSVPADCLEAAQQLRNSSLIG
48614    51 CQADPTCSAAYHHLDSCTSSISTPLPSEEPSVPADCLEAAQQLRNSSLIG

48613   101 CMCHRRMKNQVACLDIYWTVHRARSLGNYELDVSPYEDTVTSKPWKMNLS
48614   101 CMCHRRMKNQVACLDIYWTVHRARSL.....................

48613   151 KLNMLKPDSDLCLKFAMLCTLNDKCDRLRKAYGEACSGPHCQRHVCLRQL
48614   127 .......DSDLCLKFAMLCTLNDKCDRLRKAYGEACSGPHCQRHVCLRQL

48613   201 LTFFEKAAEPHAQGLLLCPCAPNDRGCGERRRNTIAPNCALPPVAPNCLE
48614   170 LTFFEKAAEPHAQGLLLCPCAPNDRGCGERRRNTIAPNCALPPVAPNCLE

48613   251 LRRLCFSDPLCRSRLVDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAM
48614   220 LRRLCFSDPLCRSRLVDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAM

48613   301 TPNFVSNVNTSVALSCTCRGSGNLQEECEMLEGFFSHNPCLTEAIAAKMR
48614   270 TPNFVSNVNTSVALSCTCRGSGNLQEECEMLEGFFSHNPCLTEAIAAKMR

48613   351 FHSQLFSQDWPHPTFAVMAHQNENPAVRPQPWVPSLFSCTLPLILLLSLW
48614   320 FHSQLFSQDWPHPTFAVMAHQNENPAVRPQPWVPSLFSCTLPLILLLSLW
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FIG. 4

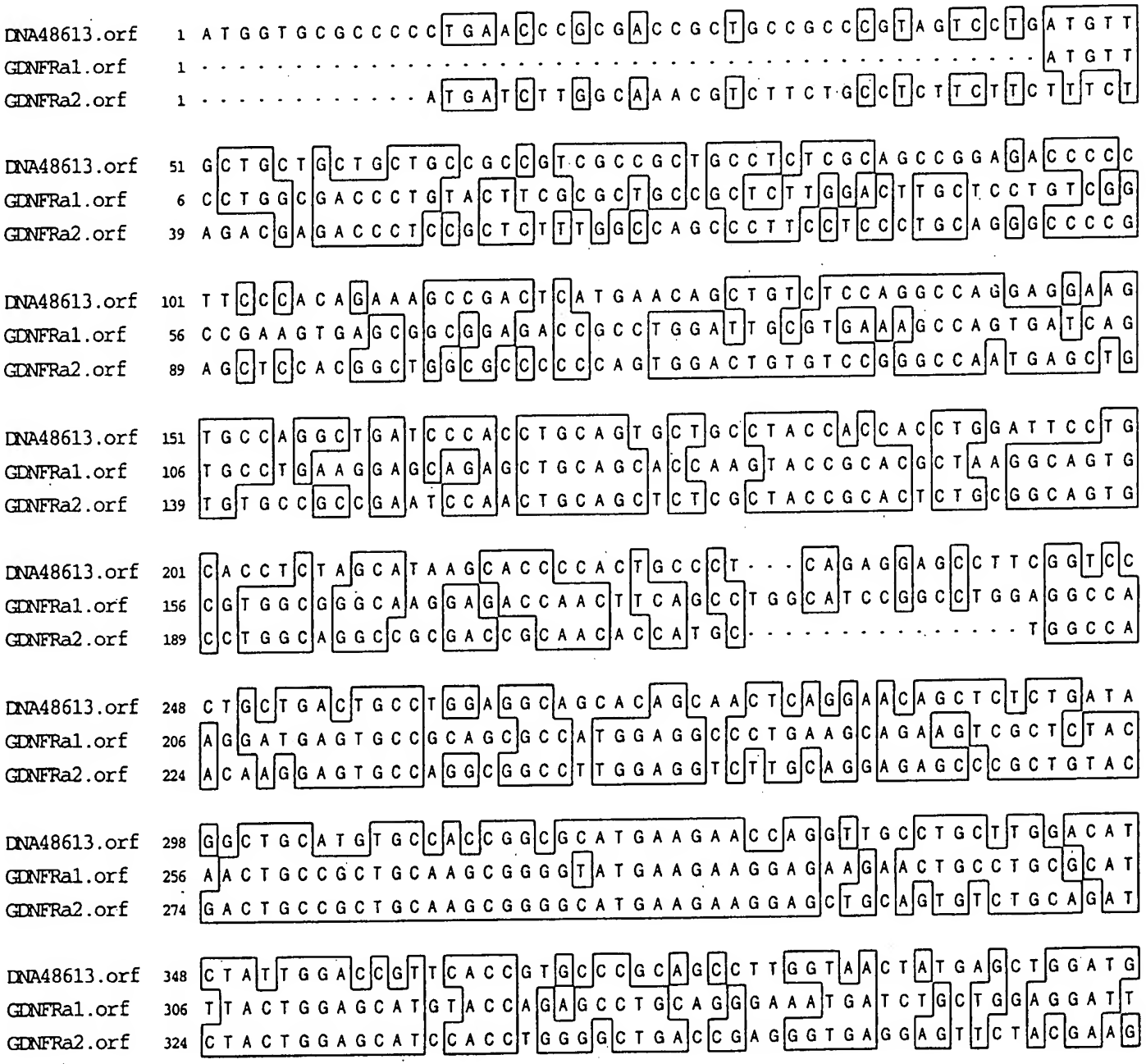


FIG. 5A

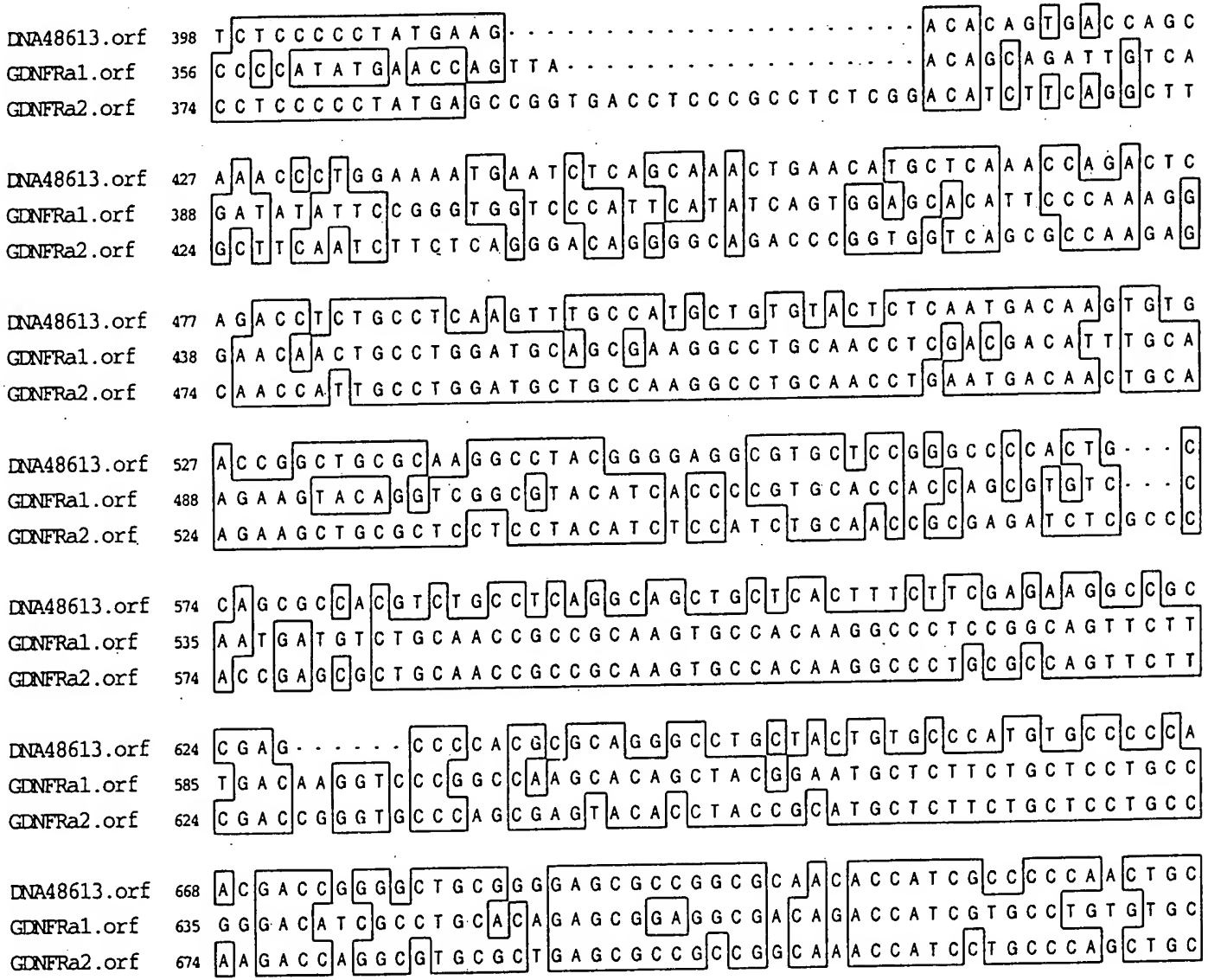


FIG. 5B

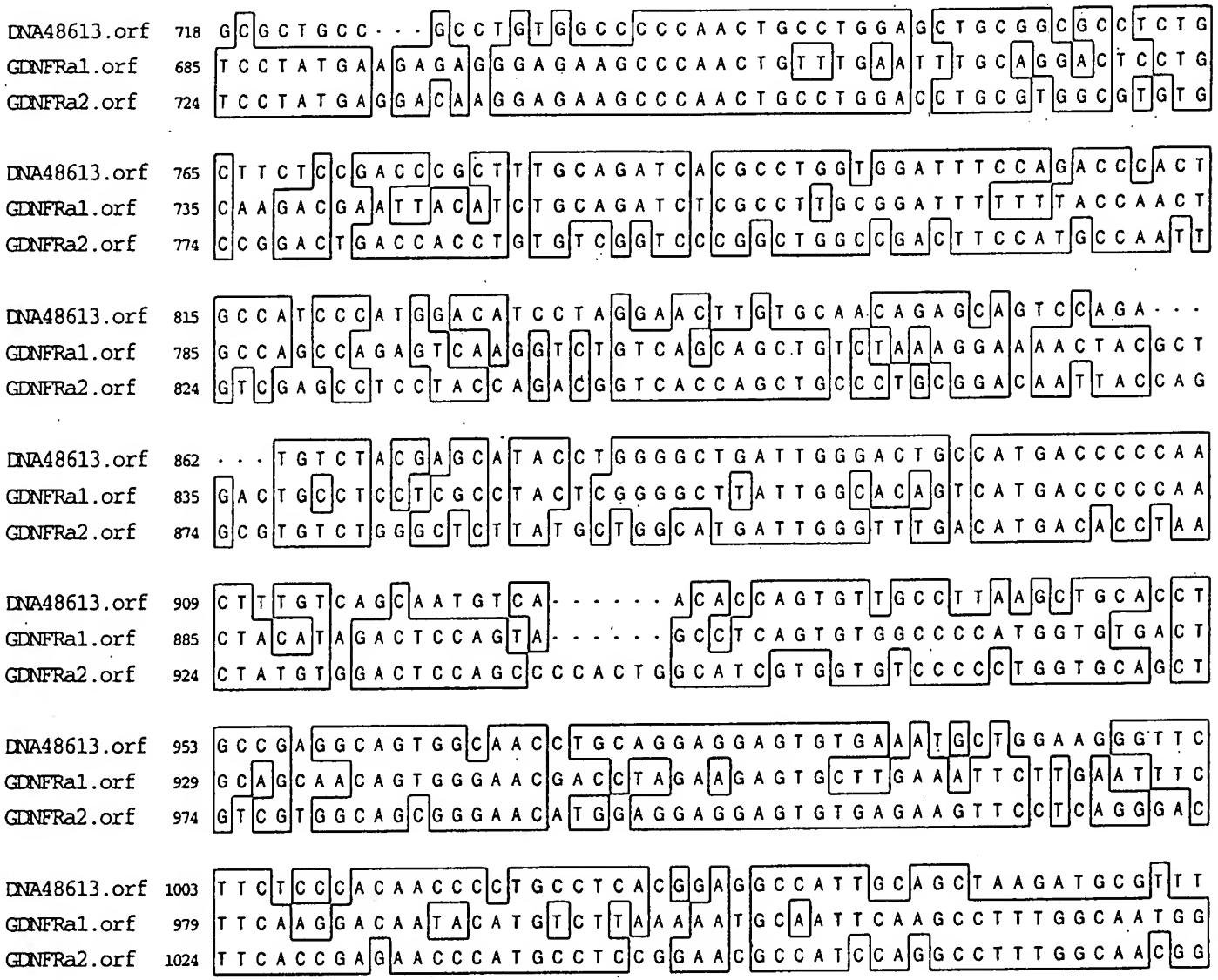


FIG. 5C

```
DNA48613.orf  1053 TCACAGCCAACTCTTCTCCCAGGACTGGCCACACCCTACCTTTGCTGTGA
GDNFRa1.orf   1029 CTCCGATGTGACCGTGTGGCAGCCAGCCTTCCCAGTACAGACCACCACTG
GDNFRa2.orf   1074 CACGGACGTGAACGTGTCCCCAAAAGGCCCCTCGTTCCAGGCCACCCAGG

DNA48613.orf  1103 TGGCACACCAGAATGAAAACCCTGCTGTGAGGCCACAGCCCTGGGTGCCC
GDNFRa1.orf   1079 CCACTACCACCACTGCCCTCCGGGTTAAGAACAAACCCTGGGGCCAGCA
GDNFRa2.orf   1124 CCCCTCGGGTGGAGAAGACGCCTTCTTGCCAGATGACCTCAGTGACAGT

DNA48613.orf  1153 TCTCTTTCTCCTGCACGCTTCCCTTGATTCTGCTCCTGAGCCTATGGTA
GDNFRa1.orf   1129 GGGTCTGAGAATGAAATTCCCACTCATGTTTTGCCACCGTGTGCAAATTT
GDNFRa2.orf   1174 ACCAGCTTGGGGACCAGTGTCATCACCACCTGCACGTCTGTCCAGGAGCA

DNA48613.orf  1203 G-------------------------------------------------
GDNFRa1.orf   1179 ACAGGCACAGAAGCTGAAATCCAATGTGTCGGGCAATACACACCTCTGTA
GDNFRa2.orf   1224 GGGGCTGAAGGCCAACAACTCCAAAGAGTTAAGCATGTGCTTCACAGAGC

GDNFRa1.orf   1229 TTTCCAATGGTAATTATGAAAAAGAAGGTCTCGGTGCTTCCAGCCACATA
GDNFRa2.orf   1274 TCACGACAAATATCATCCCAGGGAGTAACAAGGTGATCAAACCTAACTCA

GDNFRa1.orf   1279 ACCACAAAATCAATGGCTGCTCCTCCAAGCTGTGGTCTGAGCCCACTGCT
GDNFRa2.orf   1324 GGCCCCAGCAGAGCCAGACCGTCGGCTGCCTTGACCGTGCTGTCTGTCCT

GDNFRa1.orf   1329 GGTCCTGGTGGTAACCGCTCTGTCCACCCTATTATCTTTAACAGAAACAT
GDNFRa2.orf   1374 GATGCTGAAACAGGCCTTGTAG-------------------------

GDNFRa1.orf   1379 CATAG
```

FIG. 5D

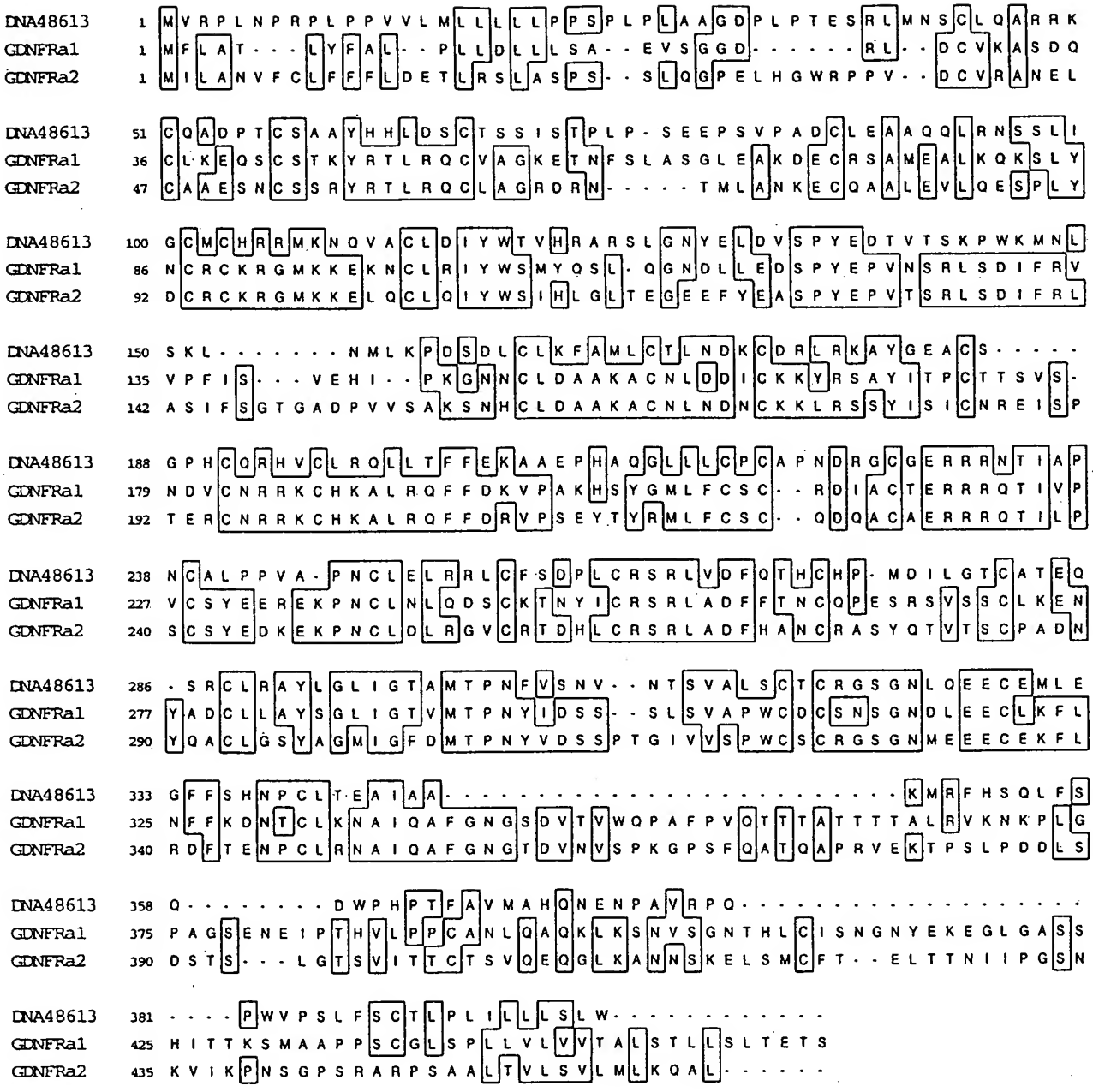


FIG. 6

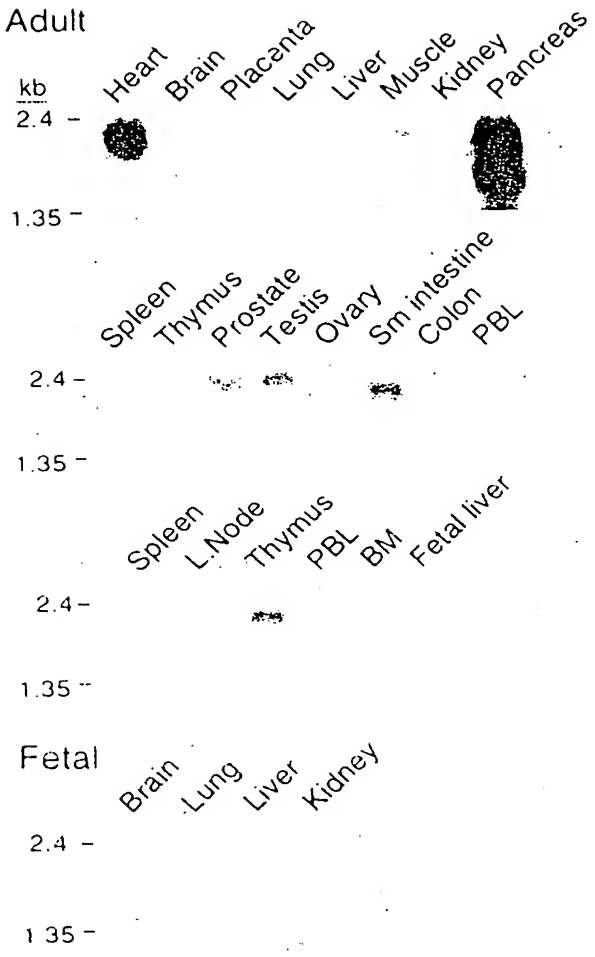


FIG. 7

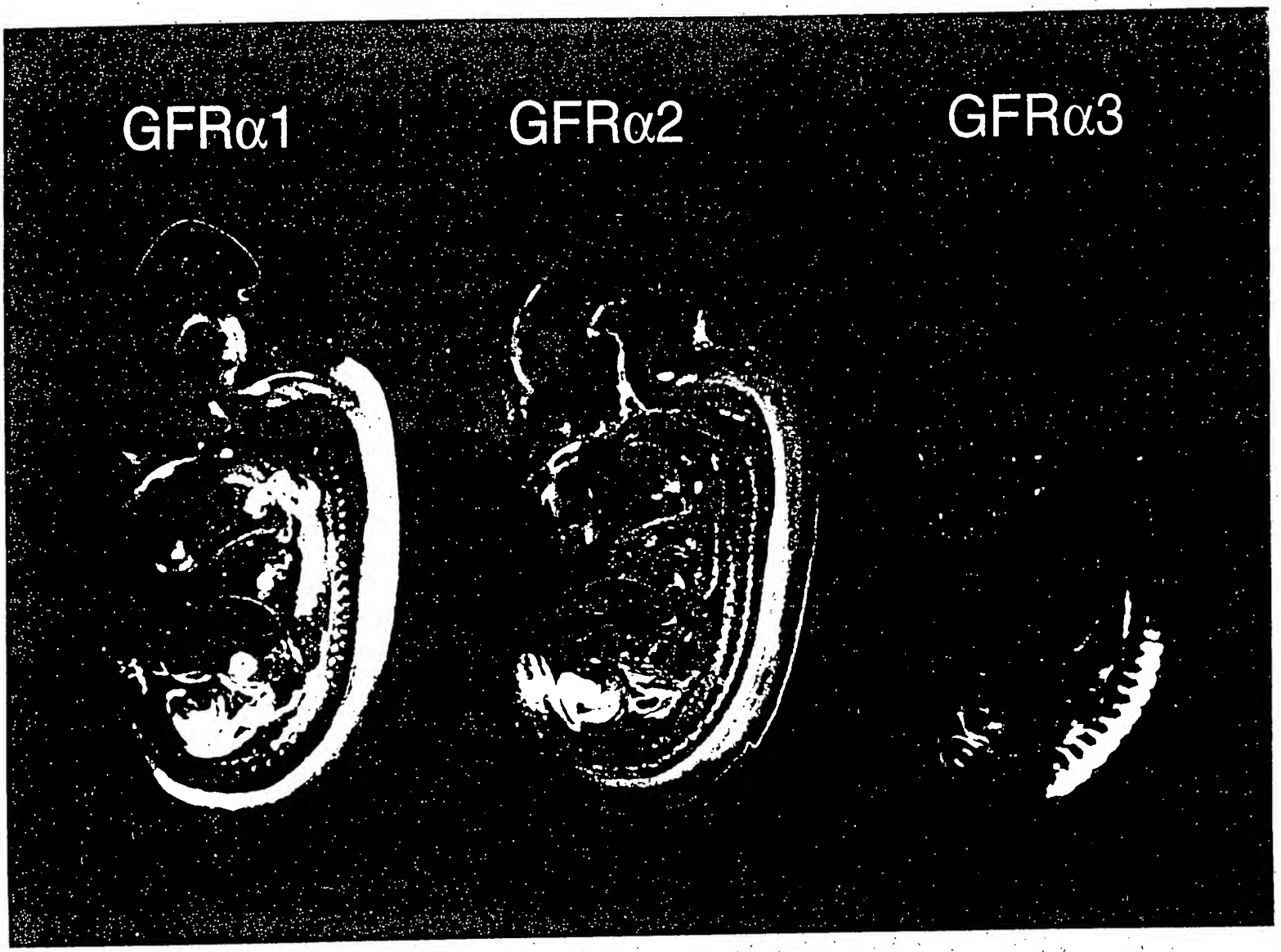


FIG. 8

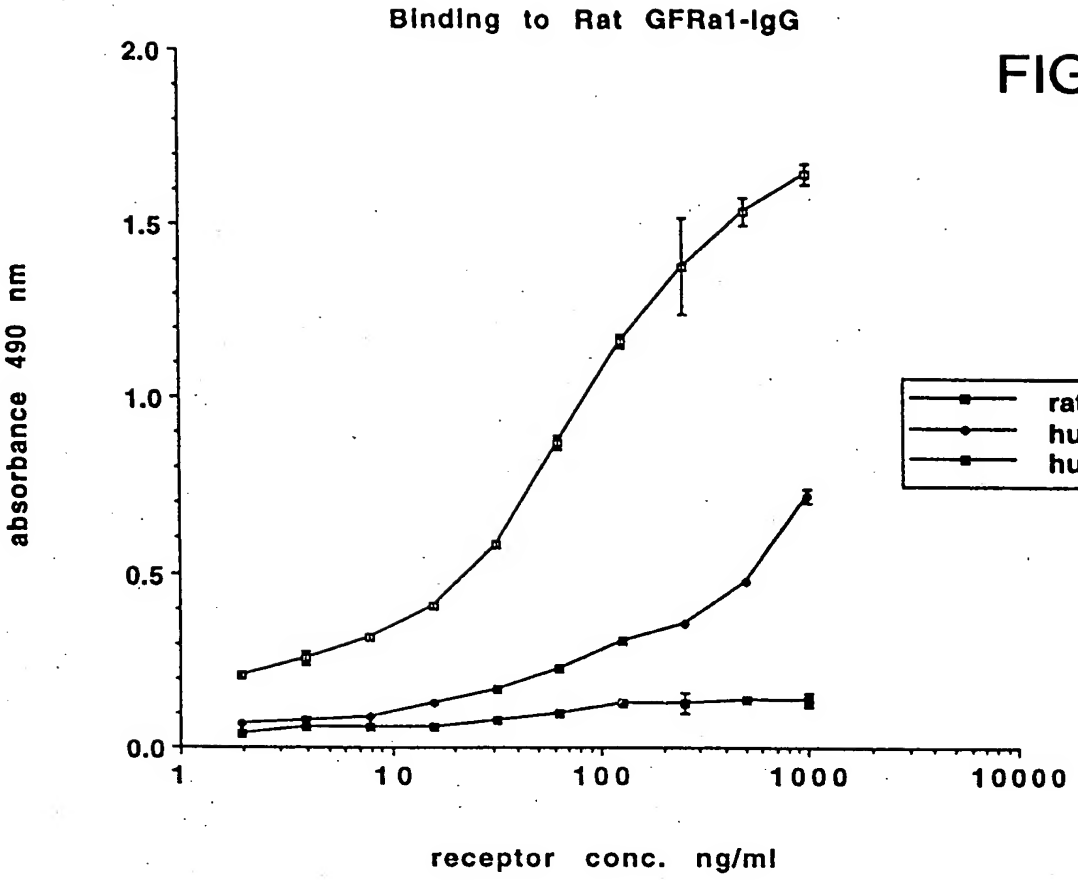


FIG. 9A

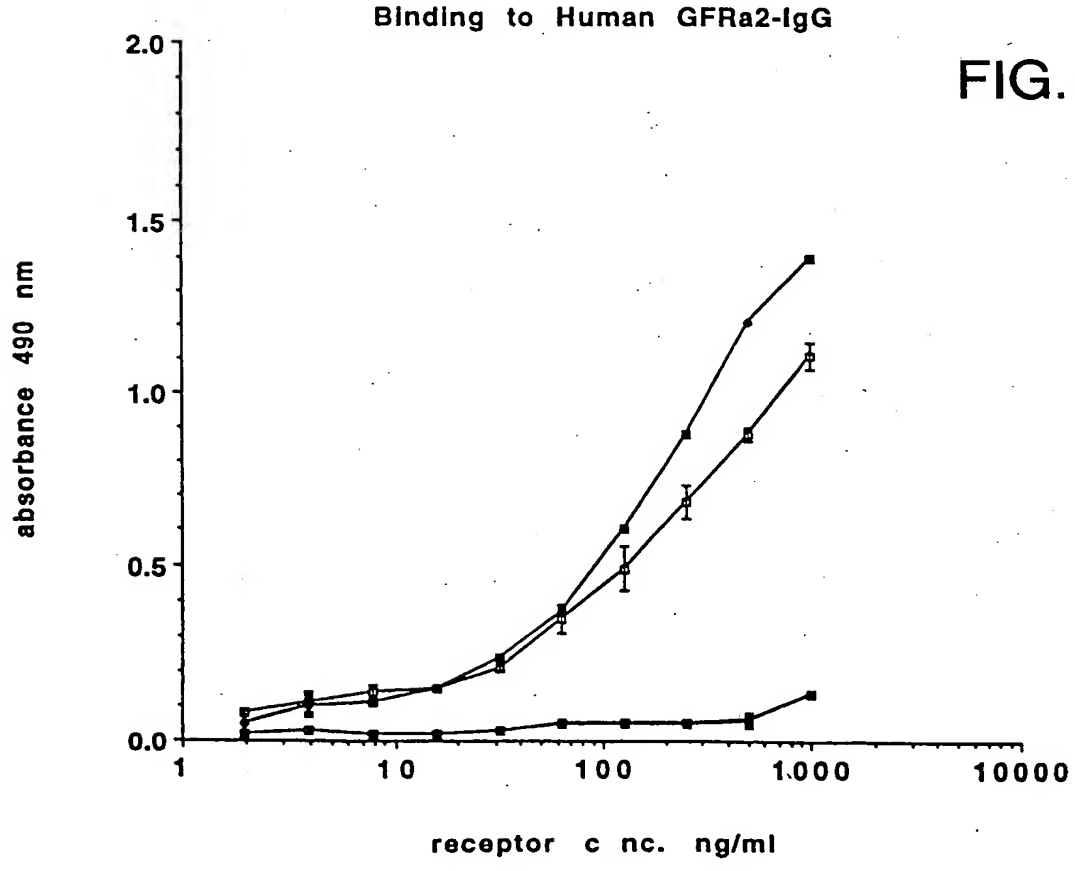


FIG. 9B

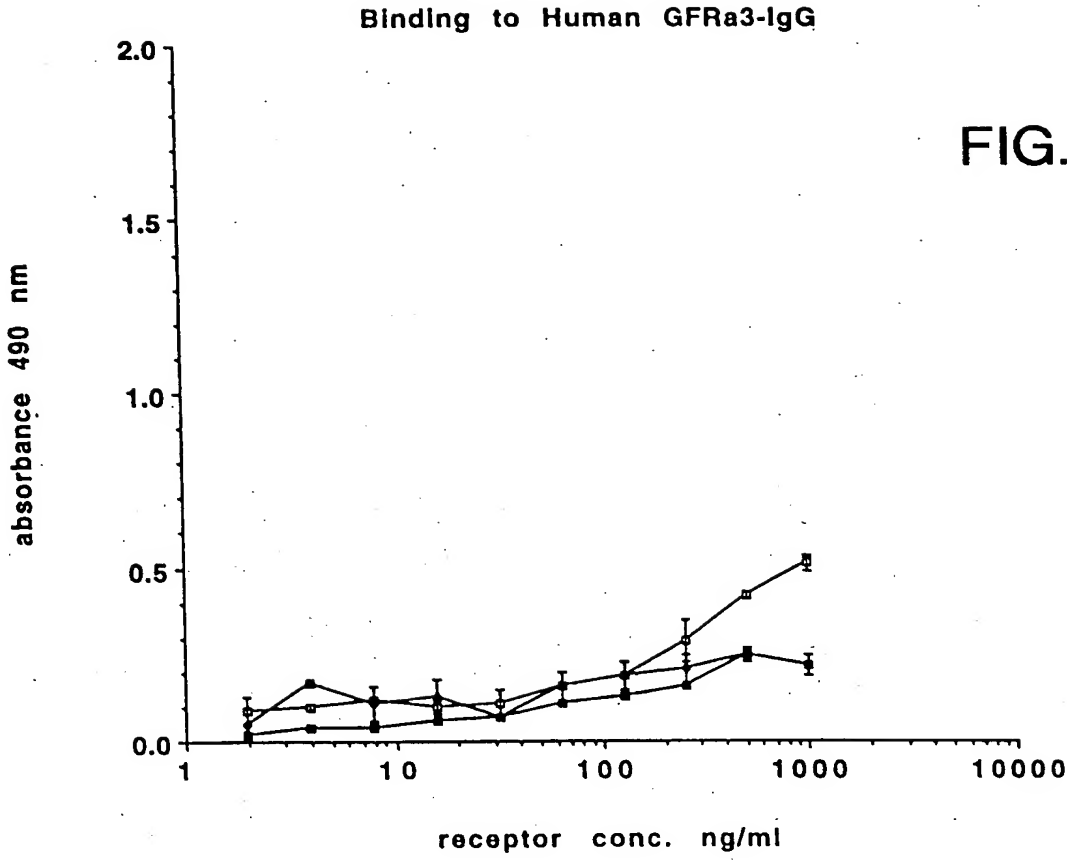


FIG. 9C

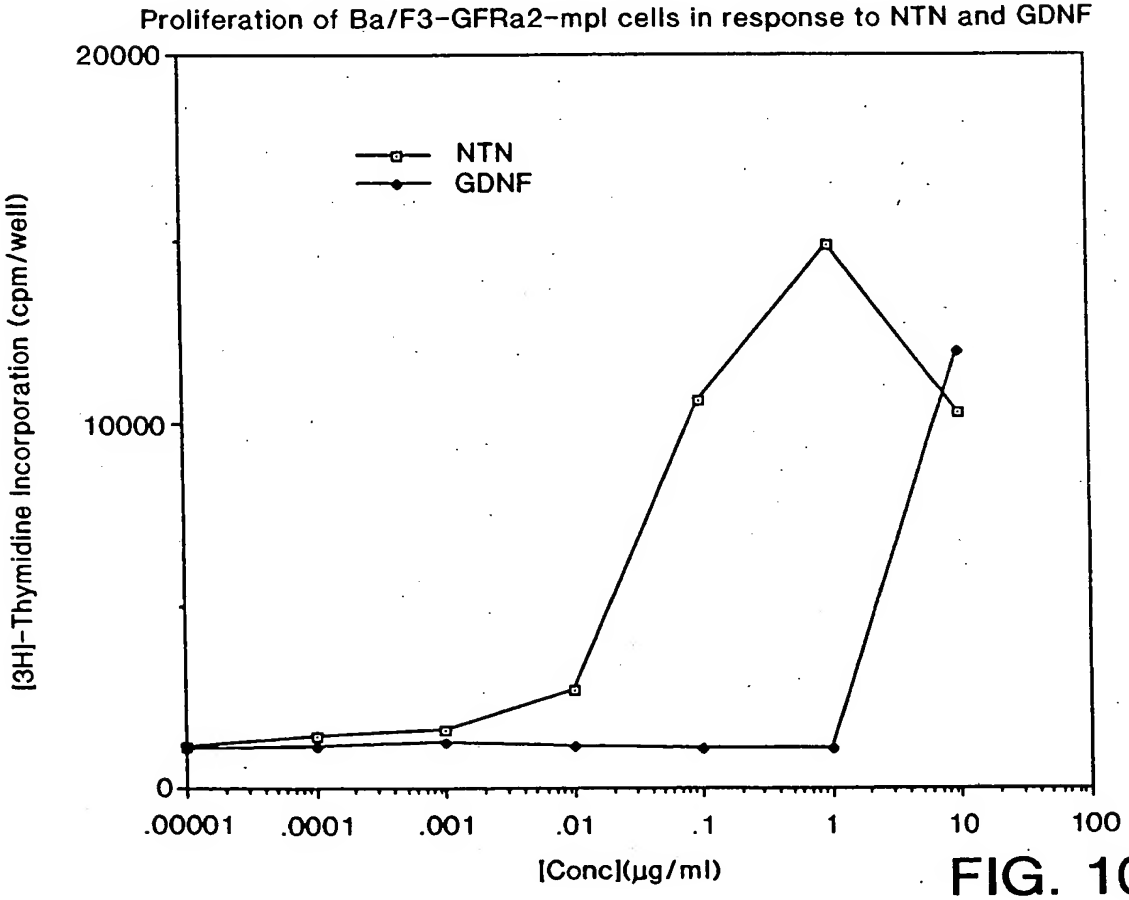


FIG. 10

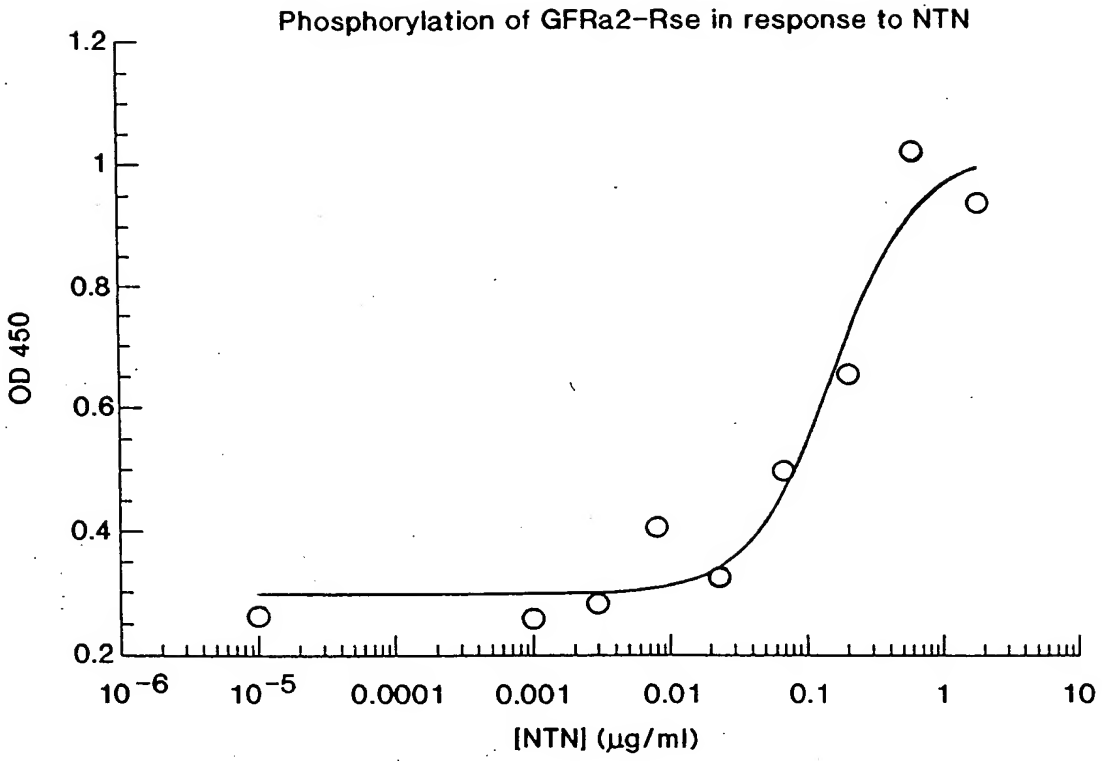


FIG. 11

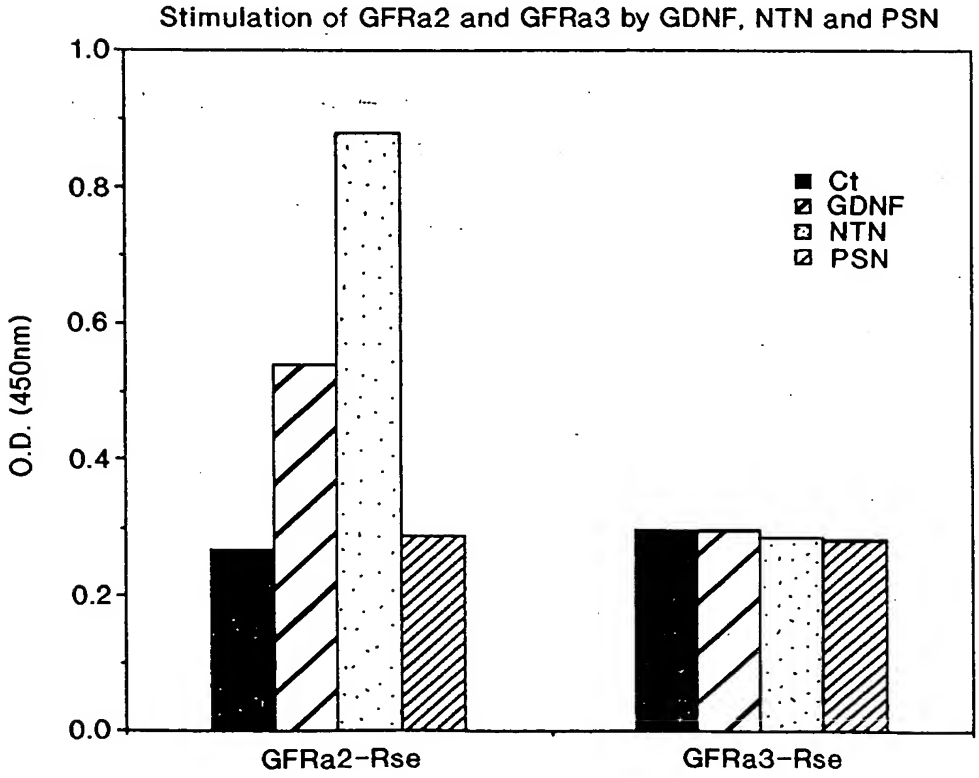
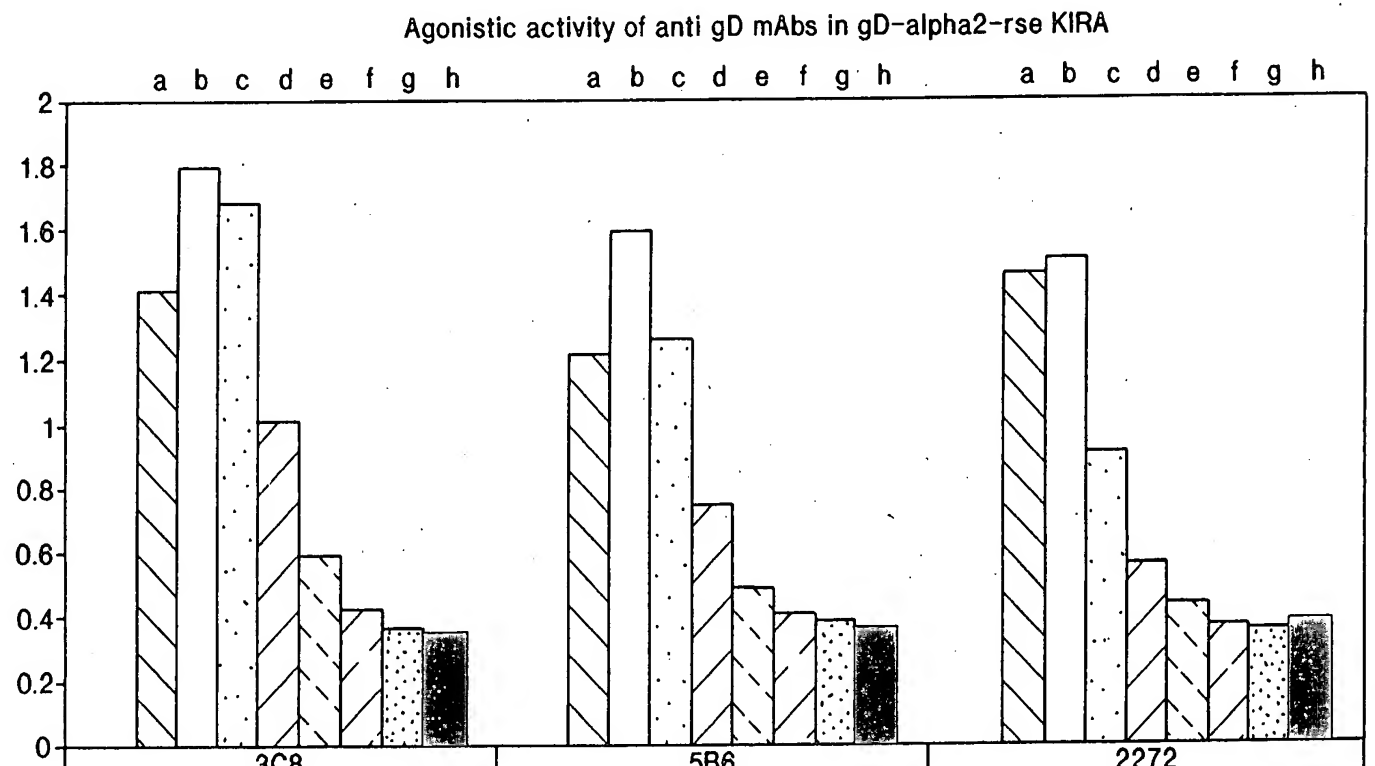


FIG. 12



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b	0.4	1.791	1.600	1.511
c	0.16	1.684	1.267	0.915
d	0.064	1.017	0.749	0.562
e	0.0256	0.589	0.490	0.439
f	0.01024	0.427	0.406	0.371
g	0.004096	0.370	0.392	0.363
h	0	0.357	0.369	0.372

FIG. 13